

Atty. Docket No. 16517.127

Appl. No. 09/692,412

Page 2

(C) propagating and self pollinating seeds from said cross;

(D) selecting progeny of self pollinated seeds with said phenotype;

*Ai* (E) screening progeny of self pollinated seeds with said phenotype with a collection of nucleic acid molecules, said collection of nucleic acid molecules capable of detecting a set of polymorphisms where the polymorphisms are distributed throughout the genome of said self pollinated seeds with said phenotype at an average density of more than one polymorphism per about 100kb;

(F) calculating the linkage of each of said polymorphisms to said phenotype; and

(G) isolating said region of genomic DNA associated with said phenotype based on its linkage to one or more of said nucleic acid molecules.

4. (Once Amended) A method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

*Cx* (A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb;

(B) calculating the linkage of each of said polymorphisms to said phenotypic trait; and

(C) identifying said genomic DNA region associated with said phenotypic trait based on its linkage to one or more of said nucleic acid molecules.

Atty. Docket No. 16517.127

Appl. No. 09/692,412

Page 3

6. (Once Amended) The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said collection of nucleic acid molecules is capable of detecting Single Nucleotide Polymorphism 466799.

7. (Once Amended) The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said collection of nucleic acid molecules is capable of detecting Single Nucleotide Polymorphism 471736.

10. (Once Amended) A method of isolating a nucleic acid molecule associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, wherein said polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb;

(B) calculating the linkage of each of said polymorphisms to said phenotypic trait;  
and

(C) isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

11. (Once Amended) The method of isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 466799.

Atty. Docket No. 16517.127

Appl. No. 09/692,412

Page 4

AG 12. (Once Amended) The method of isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 471736.

15. (Once Amended) The method of isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

AG 16. (Once Amended) The method of isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 0 and about 5cM of one or more of said polymorphisms.

17. (Once Amended) A method of identifying a nucleic acid molecule associated with a phenotypic trait comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100 kb; and

(B) identifying said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

Atty. Docket No. 16517.127

Appl. No. 09/692,412

Page 5

Please add new claims 27-35:

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27. (Added) The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said collection of nucleic acid molecules is capable of detecting Single Nucleotide Polymorphism 466799.

28. (Added) The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said collection of nucleic acid molecules is capable of detecting Single Nucleotide Polymorphism 471736.

29. (Added) The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said region of genomic DNA associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

30. (Added) The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said region of genomic DNA associated with said phenotypic trait is located between about 0 and about 5 cM of one or more of said polymorphisms.

31. (Added) The method of identifying a nucleic acid molecule associated with a phenotypic trait according to claim 17, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 466799.

Atty. Docket No. 16517.127

Appl. No. 09/692,412

Page 6

32. (Added) The method of identifying a nucleic acid molecule associated with a phenotypic trait according to claim 17, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 471736.

33. (Added) The method of identifying a nucleic acid molecule associated with a phenotypic trait according to claim 17, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

34. (Added) The method of identifying a nucleic acid molecule associated with a phenotypic trait according to claim 17, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 0 and about 5 cM of one or more of said polymorphisms.

35. (Added) The method of identifying a nucleic acid molecule associated with a phenotypic trait according to claim 17, further comprising isolating said identified nucleic acid molecule.

#### REMARKS

Applicants thank the Examiner for the interview granted on August 16, 2001, and for the comments and suggestions provided at that time. In response to the interview, Applicants submit the following remarks.